

FIGURE 1A

1	GAATTTGGCC	CTCGAGGCCA	AGAAATTCGGC	ACGAGGCGCG	GCGCCACAGC	CAGGCAGAGC	GCTGTGCGCAT	CCCGGCGGTC	CACCCGCCAT	GGGGCTCTCC
1	CTTAAACCGG	GAGCTCCGGT	TCTTAAGCCG	TGCTCCGCGC	CGCGGTCTCG	GTCCGTCTCG	CGACAGCGTA	GGGCCGCGAG	GTGGCGGTA	CCCCGAGAGG
									Me	tglyLeuSer
101	TGGAGCCCGC	GACCTCCACT	GCTGATGATC	CTGCTACTGG	TGCTGTCTGT	GTGGCTGCCA	CTTTGGAGCAG	GAACCTCCCT	TGCCACAGAG	AACAGTTTGG
	ACCTCGGCGG	CTGGAGGTGA	CGACTACTAG	GACGATGACC	ACGACAGCAA	CACCGACGGT	GAACCTCGTC	CTTTGAGGGA	ACGGTGTCTC	TTGTCCAAAC
5	TrpSerProA	rgProProLe	uLeuMetIle	LeuLeuLeuV	alleuSerLe	uTrpLeuPro	LeuGlyAlaG	lyAsnSerLe	uAlaThrGlu	AsnArgPheVal
201	TGAACAGCTG	TACCAGGCC	AGAAAGAAAT	GCGAGGCTAA	TCCCGTTTGC	AAGGCTGCCT	ACCAGACCTT	GGGCTCTGTC	ACCTCCAGTT	TAAGCAGGCC
	ACTTGTGAC	ATGGGTCCGG	TCTTTCTTTA	CGCTCCGATT	AGGGGAACG	TTCCGACGGA	TGGTCTGGA	CCCCAGGACG	TGGAGGTCAA	ATTCTGCCGG
39	AsnSerCy	sThrGlnAla	ArgLysLysC	ysGluAlaAs	nProAlaCys	LysAlaAlaT	yrGlnHisLe	uGlySerCys	ThrSerSerL	euSerArgPro
301	GCTGCCCTTA	GAGGAGTCTG	CCATGTCTGC	AGACTGCCTA	GAGGACGACG	AACAACTCAG	GAACAGCTCT	CTGATAGACT	GCAGGTGCCA	TCGGCGCATG
	CGACGGGAAT	CTCCTCAGAC	GGTACAGACG	TCTGACGGAT	CTCCGTCTGC	TTGTGTGAGTC	CTTTGTCGAGA	GACTATCTGA	CGTCCACGGT	AGCCGCGTAC
72	LeuProLeu	GluGluSera	laMetSerAl	aAspCysLeu	GluAlaAlaG	luGlnLeuAr	gAsnSerSer	LeulleAspC	ysArgCysHi	sArgArgMet
401	AAGCACAAG	CTACCTGTCT	GGACATTTAT	TGGACCGTTC	ACCCTGCCCG	AAGCCTTGGT	GACTACGAGT	TGGATGTCTC	ACCCTATGAA	GACACACTGA
	TTCTGTGTTTC	GATGGACAGA	CCTGTAAATA	ACCTGGCAAG	TGGGACGGGC	TTCCGAACCA	CTGATGCTCA	ACCTACAGAG	TGGGATACTT	CTGTGTCACT
105	LysHisGlnA	laThrCysLe	uAspIleTyr	TrpThrValH	isProAlaAr	gSerLeuGly	AspTyrGluL	euAspValSe	rProTyrGlu	AspThrValThr
501	CCAGCAAAAC	CTGGAAAATG	AATCTTAGCA	AGTTGAACAT	GCTCAAAACA	GACTCGGACC	TCTGCCTCAA	ATTTCTCTATG	CTGTGTACTC	TTCCAGACAA
	GGTCGTTTGG	GACCTTTTAC	TTAGATCTGT	TCAACTTTGT	CGAGTTTGGT	CTGAGCTGG	AGACGAGTT	TAAACGATAC	GACACATGAG	AAGTGTGTGT
139	SerLysPr	oTrpLysMet	AsnLeuSerL	ysLeuAsnMe	tLeuLysPro	AspSerAspL	euCysLeuLy	sPheAlaMet	LeuCysThrL	euHisAspLys
601	GTGTGACCGC	CTGCGCAAGG	CCTACGGGGA	GGCATGCTCA	GGATCCGCT	GCCAGCGCCA	CCTCTGCCCTA	GCCCAGCTGC	GCTCCTTCTT	TGAGAAGGCA
	CACACTGGCG	GACGGGTTCC	GGATGCCCTT	CCGTACGAGT	CCCTAGGCGA	CGGTCCGGT	GGAGACGGAT	CGGTCGACG	CGAGGAAGAA	ACTCTTCCGT
172	CysAspArg	LeuArgLysA	laTyrGlyG	uAlaCysSer	GlyIleArgC	ysGlnArgHi	sLeuCysLeu	AlaGlnLeuA	rgSerPhePh	eGluLysAla
701	GCAGAGTCCC	ACGCTCAGGG	TCTGTCTGCTG	TGTCCCTGTG	CACCAGAAGA	TGCGGGCTGT	GGGAGCGGC	GGCGTAACAC	CATCGCCCCC	AGTTGGGCCC
	CGTCTCAGGG	TGCGAGTCCC	AGACGACGAC	ACAGGACAC	GTGGTCTTCT	ACGCCGACA	CCCCTCGCCG	CCGATTTGTG	GTAGCGGGG	TCAACGCGGG
205	AlaGluSerH	isAlaGlnG	lYLeuLeuLeu	CysProCysA	laProGluAs	pAlaGlyCys	GlyGluArgA	rgArgAsnTh	rIleAlaPro	SerCysAlaLeu
801	TGCCCTTCTGT	AACCCCAAT	TGCCCTGGATC	TGCGGAGCTT	CTGCCGTGCG	GACCCCTTGT	GCAGATCACC	CCTGATGGAC	TTCCAGACCC	ACTGTCTATCC
	ACGGAAGACA	TTGGGGTTA	ACGGACCTAG	ACGCCCTGAA	GACGGACGCG	CTGGGAACA	CGTCTAGTGC	GGACTACCTG	AAGGTCTGGG	TGACACTAGG
239	ProSerVa	lThrProAsn	CysLeuAspL	euArgSerPh	eCysArgAla	AspProLeuC	ysArgSerAr	gLeuMetAsp	PheGlnThrH	isCysHisPro
901	TATGACATC	CTTGGGACTT	GTGCAACTGA	GCAGTCCAGA	TGTCTGCGGG	CATACCTGGG	GCTGATTTGG	ACTGCCATGA	CCCCAAACTT	CATCAGCAAG
	ATACCTGTAG	GAACCTGAA	CACGTTGACT	CGTCAAGTCT	ACAGACGCCC	GTATGACCCC	CGACTAACCC	TGACGCTACT	GGGGTTTGA	GTAGTCTTTC
272	MetAspIle	LeuGlyThrC	ysAlaThrG	uGlnSerArg	CysLeuArgA	laTyrLeuG	ylleuileGly	ThrAlaMetT	hrProAsnPh	eIleSerLys

[illegible]

FIGURE 2

hGFra3 1 MVRP L N P R P L P P V V L M L L L L L P P S P L P L A A G D P L P T E S R L M N S C L Q A R R K
mGFra3 1 - - M G L S W S P R P P L L M I L L L V L S L W - L P L G A G N S L A T E N R F V N S C T Q A R K K

hGFra3 51 C Q A D P T C S A A Y H H L D S C T S S I S T P L P S E E P S V P A D C L E A A Q Q L R N S S L I G
mGFra3 48 C E A N P A C K A A Y Q H L G S C T S S L S R P L P L E E S A M S A D C L E A A E Q L R N S S L I D

hGFra3 101 C M C H R R M K N Q V A C L D I Y W T V H R A R S L G N Y E L D V S P Y E D T V T S K P W K M N L S
mGFra3 98 C R C H R R M K H Q A T C L D I Y W T V H P A R S L G D Y E L D V S P Y E D T V T S K P W K M N L S

hGFra3 151 K L N M L K P D S D L C L K F A M L C T L N D K C D R L R K A Y G E A C S G P H C Q R H V C L R Q L
mGFra3 148 K L N M L K P D S D L C L K F A M L C T L H D K C D R L R K A Y G E A C S G I R C Q R H L C L A Q L

hGFra3 201 L T F F E K A A E P H A O G L L L C P C A P N D R G C G E R R R N T I A P N C A L P P V A P N C L E
mGFra3 198 R S F F E K A A E S H A O G L L L C P C A P E D A G C G E R R R N T I A P S C A L P S V T P N C L D

hGFra3 251 L R R L C F S D P L C R S R L V D F Q T H C H P M D I L G T C A T E Q S R C L R A Y L G L I G T A M
mGFra3 248 L R S F C R A D P L C R S R L M D F Q T H C H P M D I L G T C A T E Q S R C L R A Y L G L I G T A M

hGFra3 301 T P N F V S N V N T S V A L S C T C R G S G N L O E E C E M L E G F F S H N P C L T E A I A A K M R
mGFra3 298 T P N F I S K V N T T V A L S C T C R G S G N L O D E C E Q L E R S F S Q N P C L V E A I A A K M R

hGFra3 351 F H S Q L F S Q D W P H P T F A V M A H Q N E N P A V R P Q P W V P S L F S C T L P L I L L L S L W
mGFra3 348 F H R Q L F S Q D W A D S T F S V V Q Q Q N S N P A L R L Q P R L P I L S F S I L P L I L L Q T L W

fig 4

FIGURE 3

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48613      1  MVRPLNPRPLPPVVLMLLLLLPPSPLPLAAGDPLPTESRLMNSCLOARRK
48614      1  MVRPLNPRPLPPVVLMLLLLLPPSPLPLAAGDPLPTESRLMNSCLOARRK

48613     51  CQADPTCSAAYHHLD SCTSSISTPLPSEEPSVPADCLEAAQQLRNSSLIG
48614     51  CQADPTCSAAYHHLD SCTSSISTPLPSEEPSVPADCLEAAQQLRNSSLIG

48613    101  CMCHRRMKNQVACLDIYWTVHRARSLGNYELDVSPYEDTVTSKPWKMNLS
48614   -101- CMCHRRMKNQVACLDIYWTVHRARSL.....

48613    151  KLNMLKP DSDLCLKFAMLC TLNDKCDRLRKAYGEACSGPHCQRHVCLROL
48614    127  ..... DSDLCLKFAMLC TLNDKCDRLRKAYGEACSGPHCQRHVCLROL

48613    201  LTFFEKAAEPHAOGLLLCPCAPNDRGCGERRRNTIAPNCALPPVAPNCLE
48614    170  LTFFEKAAEPHAOGLLLCPCAPNDRGCGERRRNTIAPNCALPPVAPNCLE

48613    251  LRRLCFSDPLCRSRLVDFOTHCHPMDILGTCATEQSRLCLRAYLGLIGTAM
48614    220  LRRLCFSDPLCRSRLVDFOTHCHPMDILGTCATEQSRLCLRAYLGLIGTAM

48613    301  TPNFVSVNVT SVALSCTCRGSGNLQEECEMLEGFFSHNPCLTEAIAAKMR
48614    270  TPNFVSVNVT SVALSCTCRGSGNLQEECEMLEGFFSHNPCLTEAIAAKMR

48613    351  FHSQLFSQDWPHTFAVMAHONENPAVRPQPWVPSLFSCTLPLILLLSLW
48614    320  FHSQLFSQDWPHTFAVMAHONENPAVRPQPWVPSLFSCTLPLILLLSLW

```

FIGURE 4

[illegible]

DNA48613.orf 718 GCGCTGCC...GCTGTGGCCCCCAACTGCCTGGA GCTGCGGCGGCCTCTG
GDNFRa1.orf 685 TCCTATGAAGAGAGGGAGAAAGCCCAACTGTTTGAAATTIGCAGGACTCCTG
GDNFRa2.orf 724 TCCTATGAAGAGCAAAGAGAAAGCCCAACTGCCTGGA CTTGCGTGGCGTGTG

DNA48613.orf 765 CTTCCTCGGACCGCTTTGTCAGATCA CGCCTGGTGGATTTCAGACCCTACT
GDNFRa1.orf 735 CAAGACGAATTACATCTGTCAGATCTCGCCTTGGCGATTTTTACCCTACT
GDNFRa2.orf 774 CCGGACTGACCCACTGTGTCTGTCTCGGCTGGCCGACTTCCATGCCAATT

DNA48613.orf 815 GCCATCCCATGGACATCCTAGGAACCTGTGCAACAGAGCAAGTCCAGA...
GDNFRa1.orf 785 GCCAGCCAGAGTCAAGGCTGTGTCAGCAGCTGTCTAAAGGAATACTACGCT
GDNFRa2.orf 824 GTCTGAGCCTCTCTACCAAGAGGTCAACAGCTGCCCTGGGACAATTACCAAG

DNA48613.orf 862 ...TGCTCTACGAGCATACCTGGGGCTGATTGGGACTG C CATGACCCCAAA
GDNFRa1.orf 835 GACTGCTCTCTCGCCTACTCTGGGGCTTATTGGCAGAGT CATGACCCCAAA
GDNFRa2.orf 874 GCGTGTCTGGGCTCTTATGCTGGCATGATTGGGTTTGACATGACACCTAA

DNA48613.orf 909 CTTTGT CAGCAATGTCA...ACACCAAGTGTGCCCTTAAGCTGCACTCT
GDNFRa1.orf 885 CTACATAGACTCCAGTA...GCTCAGTGTGGCCCATGGTGTGACT
GDNFRa2.orf 924 CTATGTGACTCCAGCCCACTGGCATCTGTGGTGTCCCCCTGGTGCAGCT

DNA48613.orf 953 GCCGAGGCGAGTGGCAACCTGTCAGGAGGAGTGTGAATATGCTGGAAAGGGTTC
GDNFRa1.orf 929 GCAAGCAACAGTGGGAACGACCTAGAAAGAGTGTGAAATTCTTGAAATTTC
GDNFRa2.orf 974 GTCTGTGGCAGCGGGGAACATGAGAGGAGGAGTGTGAGAAAGTTCCTCAGGAGC

DNA48613.orf 1003 TTTCTCCCAACAACCCCTGCCTCACGGAGGCCATTGCAGCTAAGATGCGTTT
GDNFRa1.orf 979 TTCAAGGACAAATACATGTCTTAATAAATGCAATTCAAGCCTTTGGCAATGG
GDNFRa2.orf 1024 TTCAACCGAGAACCCATGCCTCCGGAACGCCATCAGGCTTTGGCAACGG

DNA48613.orf 1053 TCA CAGC CAACTCTTCTCCAGGACTGGCCACACCCCTACCTTTGCTGTGA
GDNFRa1.orf 1029 CTCCGATGTGACCGTGTGGCAGCCAGCCTTCCAGTACAGACCACCACTG
GDNFRa2.orf 1074 CACGGACGTGAACGTGTCCCACAAAGGCCCTCTGTTCCAGGCCACCAGG

DNA48613.orf 1103 TGGCACAACCAGAATGAAACCCCTGCTGTGAGGCCACAGCCCTGGGTGCCC
GDNFRa1.orf 1079 CCACTACCACTGCTCCCTCCGGGTTAAGAACAAACCCCTGGGGCCAGCA
GDNFRa2.orf 1124 CCCCTCTGGGTGGAAGAAGACGCTTCTTTGCCAGATGACCTCAGTGAACAGT

DNA48613.orf 1153 TCTCTTTTCTCTGCACTCTTCCCTTGATTCTGCTCTGAGCCTATGGTA
GDNFRa1.orf 1129 GGGTCTTGAGGAATGAAATCTCCACTCATGTTTGGCCACCGTGTGCAATTTT
GDNFRa2.orf 1174 ACCAGCTTGGGGACAGTGTCACTACCACTGCACGTCTGTCCAGGAGCA

DNA48613.orf 1203 G...
GDNFRa1.orf 1179 ACA GGCACAGAAAGCTGAAATCCAAATGTGTGCGGGCAATACACACCTCTGTGA
GDNFRa2.orf 1224 GGGGCTGAAGGCCAAACAATCCAAAGAGTTAAGCATGTGTCTTACAGAGG

GDNFRa1.orf 1229 TTTCAATGGTAATTATGAATAAGAAAGGTCTCGGTGCTTCCAGCCACATA
GDNFRa2.orf 1274 TCAAGACAAATACTATCCCAGGGAGTAACAAGGTGATCAAACCTAACTCA

GDNFRa1.orf 1279 ACCACAAATCAATGGCTGCTCTCCCAAGCTGTGGTCTGAGCCCACTGCT
GDNFRa2.orf 1324 GGCACCAAGCAGAGGCCAGACCGTCCGCTGCCCTTGACCGTGTGTCTGCT

GDNFRa1.orf 1329 GGTCTCTGGTGAACCGCTCTGTCCACCCTATTATCTTTAACAGAAACAT
GDNFRa2.orf 1374 GATGCTGAACACAGGCCCTTGTAG...
GDNFRa1.orf 1379 CATAG

F16JL5B

DNA48613 1 M V R P L N P R P L P P V V L M L L L L P P S P L P L A A G D P L P T E S R L M N S C L Q A R R K
GDNFRa1 1 M F L A T . . . L Y F A L . . P L L D L L L S A . . E V S G G D R L . . D C V K A S D O
GDNFRa2 1 M I L A N V F C L F F L D E T L R S L A S P S . . S L O G P E L H G W R P P V . . D C V R A N E L

DNA48613 51 C Q A D P T C S A A Y H H L D S C T S S I S T P L P . S E E P S V P A D C L E A A Q O L R N S S L I
GDNFRa1 36 C L K E Q S C S T K Y R T L R Q C V A G K E T N F S L A S G L E A K D E C R S A M E A L K Q K S L Y
GDNFRa2 47 C A A E S N C S S R Y R T L R Q C L A G R D R N T M L A N K E C O A A L E V L O E S P L Y

DNA48613 100 G C M C H R R M K N Q V A C L D I Y W T V H R A R S L G N Y E L D V S P Y E D T V T S K P W K M N L
GDNFRa1 86 N C R C K R G M K K E K N C L R I Y W S M Y Q S L . Q G N D L L E D S P Y E P V N S R L S D I F R V
GDNFRa2 92 D C R C K R G M K K E L Q C L O I Y W S I H L G L T E G E E F Y E A S P Y E P V T S R L S D I F R L

DNA48613 150 S K L N M L K P D S D L C L K F A M L C T L N D K C D R L R K A Y G E A C S
GDNFRa1 135 V P F I S . . . V E H I . . P K G N N C L D A A K A C N L D D I C K K Y R S A Y I T P C T T S V S .
GDNFRa2 142 A S I F S G T G A D P V V S A K S N H C L D A A K A C N L N D N C K K L R S S Y I S I C N R E I S P

DNA48613 188 G P H C O R H V C L R Q L L T F F E K A A E P H A O G L L L C P C A P N D R G C G E R R R N T I A P
GDNFRa1 179 N D V C N R R K C H K A L R Q F F D K V P A K H S Y G M L F C S C . . R D I A C T E R R R Q T I V P
GDNFRa2 192 T E R C N R R K C H K A L R Q F F D R V P S E Y T Y R M L F C S C . . Q D Q A C A E R R R Q T I L P

DNA48613 238 N C A L P P V A . P N C L E L R R L C F S D P L C R S R L V D F O T H C H P . M D I L G T C A T E Q
GDNFRa1 227 V C S Y E E R E K P N C L N L O D S C K T N Y I C R S R L A D F F T N C O P E S R S V S S C L K E N
GDNFRa2 240 S C S Y E D K E K P N C L D L R G V C R T D H L C R S R L A D F H A N C R A S Y Q T V T S C P A D N

DNA48613 286 . S R C L R A Y L G L I G T A M T P N F V S N V . . N T S V A L S C T C R G S G N L Q E E C E M L E
GDNFRa1 277 Y A D C L L A Y S G L I G T V M T P N Y I D S S . . S L S V A P W C D C S N S G N D L E E C L K F L
GDNFRa2 290 Y Q A C L G S Y A G M I G F D M T P N Y V D S S P T G I V V S P W C S C R G S G N M E E E C E K F L

DNA48613 333 G F F S H N P C L T E A I A A K M R F H S Q L F S
GDNFRa1 325 N F F K D N T C L K N A I Q A F G N G S D V T V W Q P A F P V Q T T T A T T T T A L R V K N K P L G
GDNFRa2 340 R D F T E N P C L R N A I Q A F G N G T D V N V S P K G P S F Q A T Q A P R V E K T P S L P D D L S

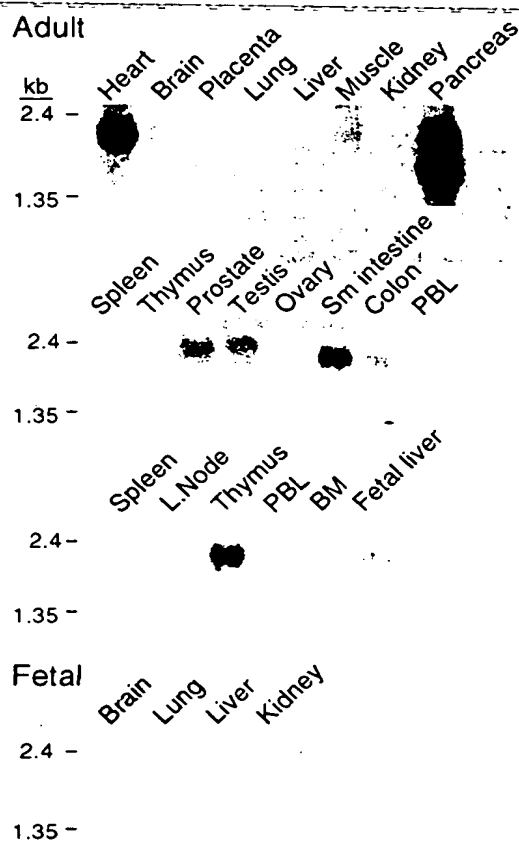
DNA48613 358 Q D W P H P T F A V M A H Q N E N P A V R P Q
GDNFRa1 375 P A G S E N E I P T H V L P P C A N L Q A O K E K S N V S G N T H L C I S N G N Y E K E G L G A S S
GDNFRa2 390 D S T S . . . L G T S V I T T C T S V Q E Q G L K A N N S K E L S M C F T . . E L T T N I I P G S N

DNA48613 381 P W V P S L F S C T L P L I L L L S L W
GDNFRa1 425 H I T T K S M A A P P S C G L S P L L V L V V T A L S T L L S L T E T S
GDNFRa2 435 K V I K P N S G P S R A R P S A A L T V L S V L M L K Q A L

FIGURE 6

protein alignment

666720 363260



NORTHERN BLOTS
FIGURE 7

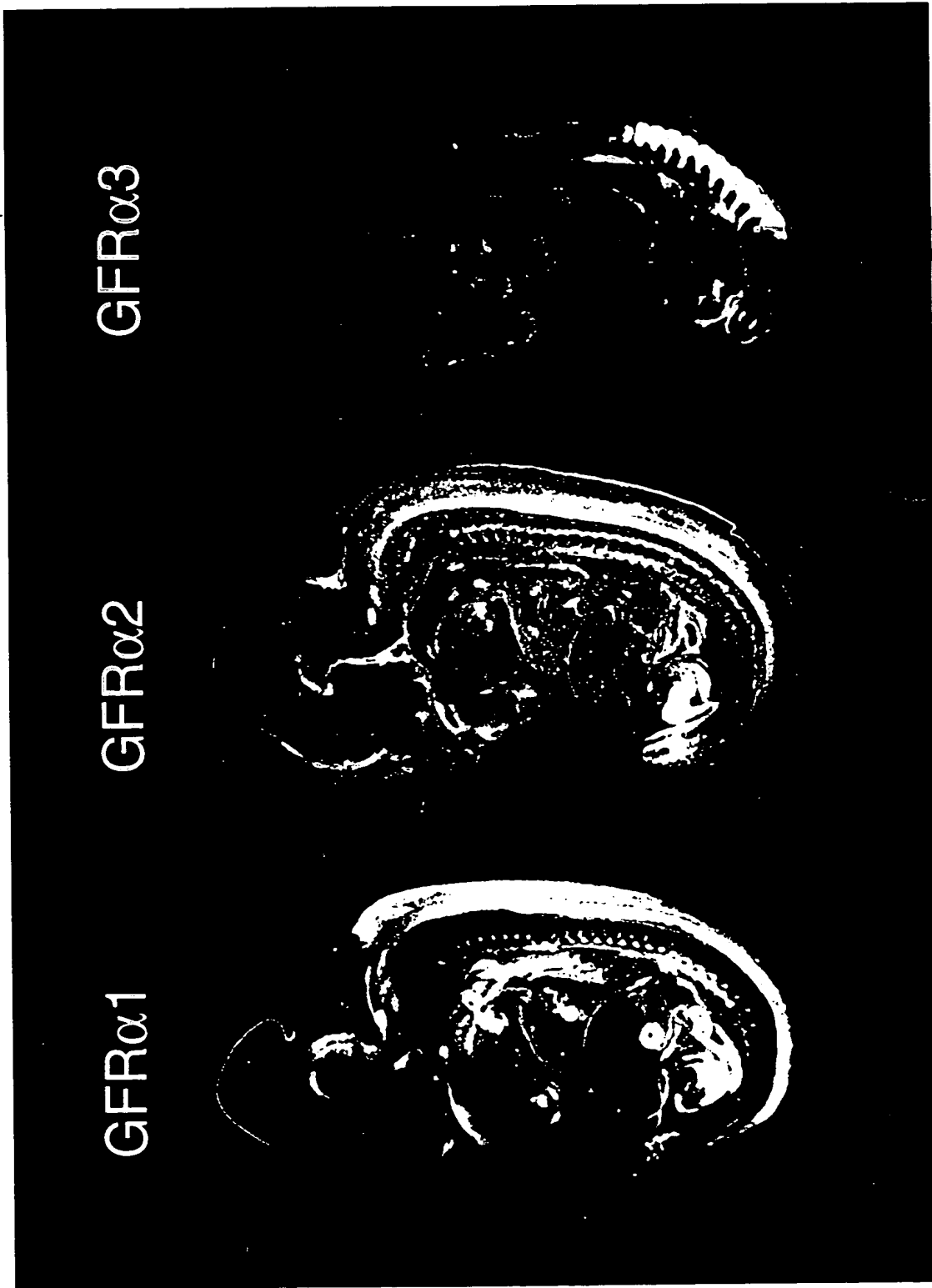


FIGURE 8

66760-563260

FIG. 9A

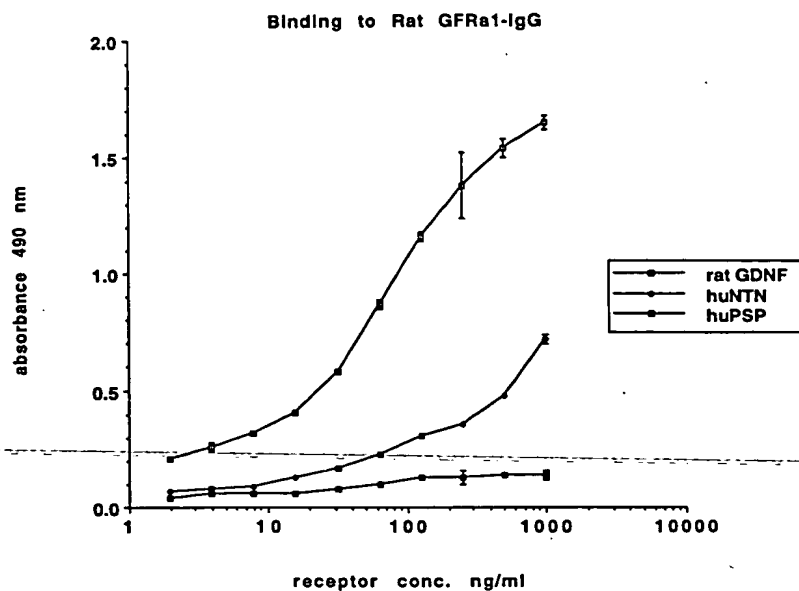


FIG. 9B

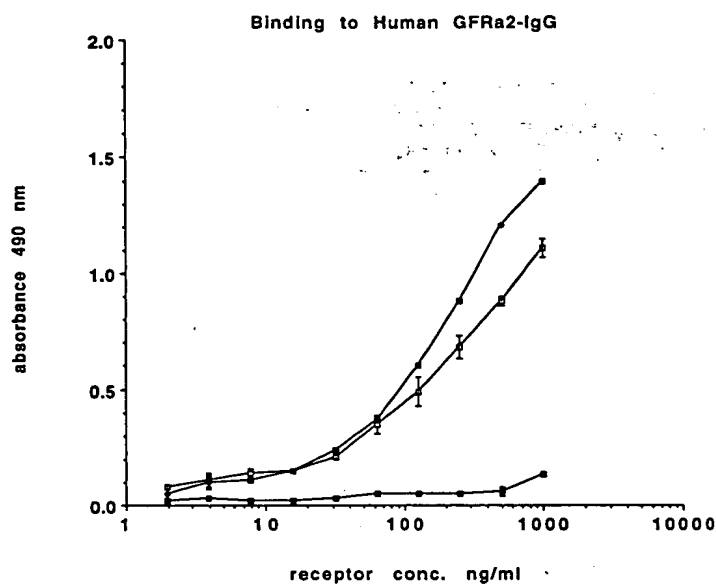
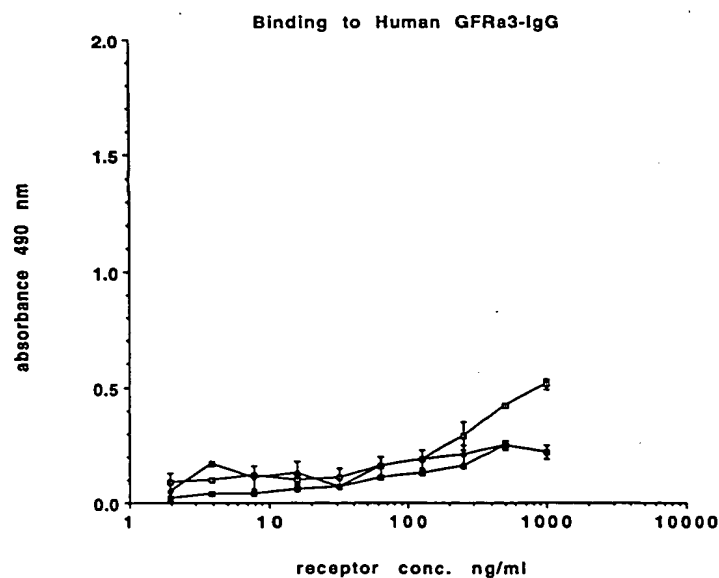


FIG. 9C



2
Proliferation of Ba/F3-GFRα₃-mpl cells in response to NTN and GDNF

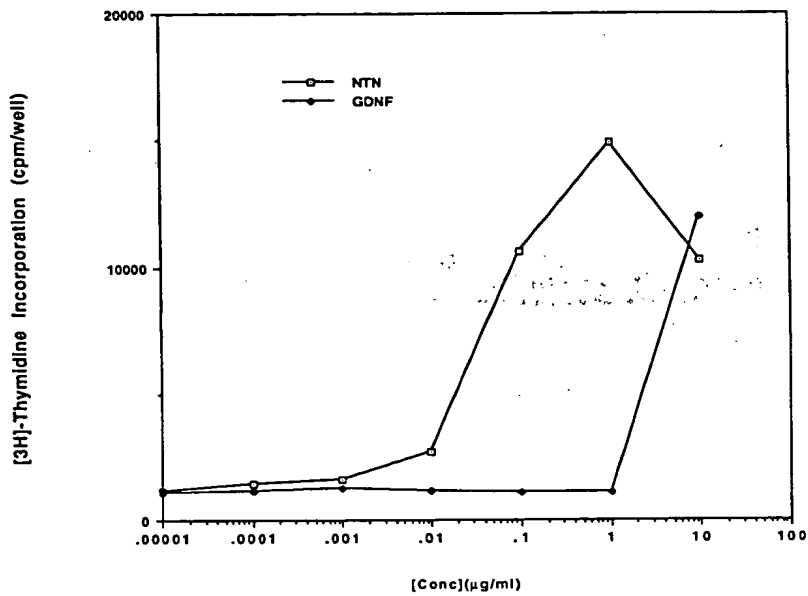


FIGURE 10

Phosphorylation of GFRa2-Rse in response to NTN

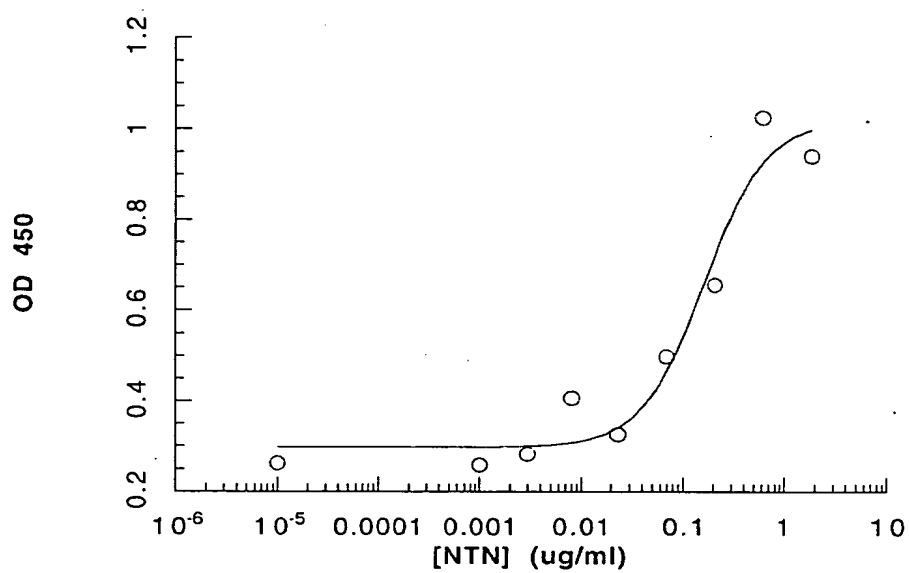


FIGURE 11

Stimulation of GFRa2 and GFRa3 by GDNF, NTN and PSN

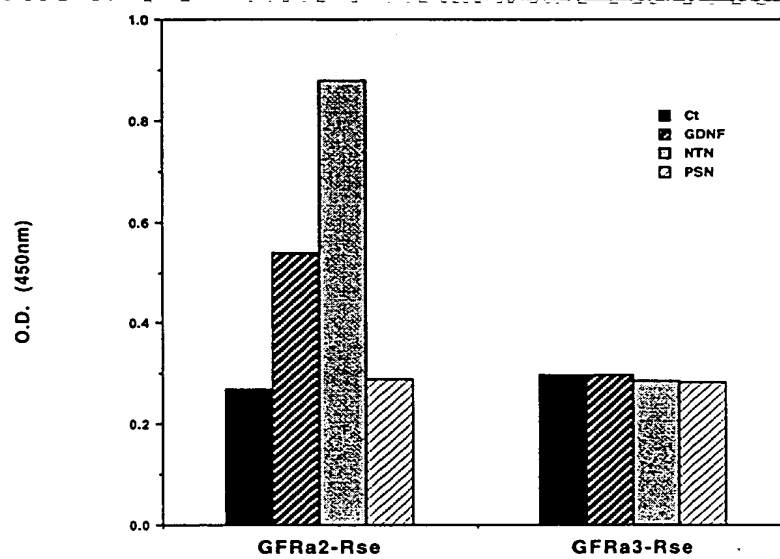
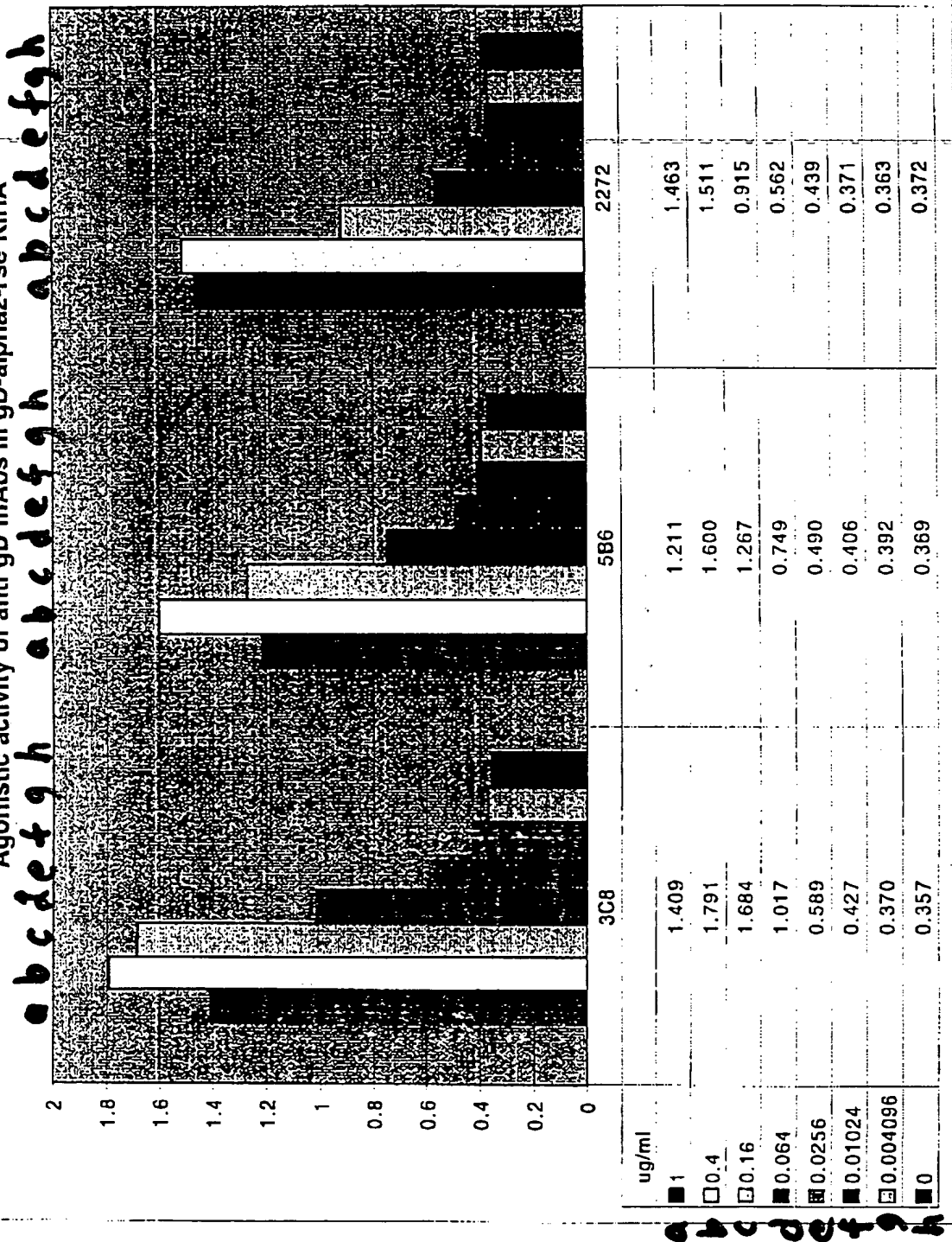


FIGURE 12

FIGURE 13

Agonistic activity of anti gD mAbs in gD-alpha2-rse KIRA



1001 GTCAACACACTA CTGTTGCCTT AAGCTGCACC TGCCGAGGCA GCGGCAACCT ACAGGACGAG TGTGACAGC TGGAAAAGGTC CTCTCTCCAG AACCCCTGCC
 CAGTTGTGAT GACAACGGAA TTTCGACGTGG ACGGCTCCGT CGCGCTTGGG TGTCCTGCTC ACATTGTCTG ACCTTTCCAG GAAGAGGGTC TTGGGGACGG
 305 ValAsnThrT hrValAlaLe uSerCysThr CysArgGlyS erGlyAsnLe uGlnAspGlu CysGluGlnL euGluArgSe rPheSerGln AsnProCysLeu
 1101 TCCTGGAGGC CATTCAGCT AAGATGCGTT TCCACAGACA GCTCTTCTCC CAGGACTGGG CAGACTCTAC TTTTTCAGTG GTGCAGCAGC AGAACAGCAA
 AGCACCTCCG GTAACGTCGA TTCTACGCAA AGGTGTCTGT CGAGAAAGAGG GTCTGAGATG AAAAAGTCAC CAGTCGTCTG TCTTGTCTGTT
 339 ValGluAl aileAlaAla LysMetArgP heHisArgG l nLeuPheSer GlnAspTrpA laAspSerTh rPheSerVal ValGlnGlnG InAsnSerAsn
 1201 CCCTGTCTCTG AGACTGCAGC CCAGGCTACC CATTTCTTCT TTCTCCATCC TTCCCTTGAT TCTGTGTCAG ACCCTCTGGT AGCTGGGGCTT CCTCAGGGTC
 GGGACGAGAC TCTGACGTG GGTCCGATGG GTAAGAAAGA AAGAGGTAGG AAGGGAACCTA AGACGACGTC TGGGAGACCA TCGACCCGAA GGAGTCCCAG
 372 ProAlaLeu ArgLeuGlnP roArgLeuPr oileLeuSer PheSerIleL euProLeuI l eLeuLeuGln ThrLeuTrp
 1301 CTTTGTCTCTC TCCACCACAC CCAGACTGAT TTGCAGCCTG TGGTGGGAGA GAACTCGCCA GCCTGTGGAA GAAGACGCAG CGTGTACAC AGCAACCCCG
 GAAACAGGAG AGGTGGTGTG GGTCTGACTA AACCTCGGAC ACCACCTCTT CTTGAGCGGT CGGACACCTT CTTCTGCGTC GCACGATGTG TCGTTGGGCC
 1401 AACCAACCAG GCATTCCGCA GCACATCCCG TCTGTCTCCAG AAGAGGTCTT AGAAGTGAGG GCTGTGACCC TTCCGATCCT GAGCGGCTAG TTTTCAAACC
 TTGGTTGGTC CGTAAGGCGT CGTGTAGGCG AGACGAGGTC TTCTCCAGAA TCTTCACTCC CGACACTGGG AAGGCTAGGA CTCGCCGATC AAAAGTTTGG
 1501 TCCCTTGCCC CTGCTTCTCTT CTGGCTCAGG CTGGTCTCC TTAGGACTTT TTGGGTCCAG TTTTGCCTTC TGTCTGTATG GTGATTAGCG GCTCACCTCC
 AGGGAACGGG GACCAAGGAA GACCGAGTCC GACGAGGAGG AATCCTGAAA CACCCAGGTC AAAACGGAAG ACAAGACTAC CACTAATCGC CGAGTGGAGG
 1601 AGCGCTTCTT CCTGTCTCCC AGGACCACCC AGAGGCTAAG GAATCAGTCA TTCCCTGTTG CTTCTCTCCAG GAAGGCAGGC TAAGGGTTCT GAGTGACTG
 TCGCGAAGAA GGACAAAGG TCCTGGTGGG TCCTCGATTC CTTAGTCACT AAGGACAAC GGAAGAGGTC CTTCCGTCCG ATTCCCAAGA CTCCTACTGAC
 1701 AGAAAAATGT TTCCTTTGTG TGGAAAGGCTG GTGCTCCAGC CTCACAGTCC CTCTGAATGG AAGATAAAAA CCTGCTGGTG TCTTGACTGC TCTGCCAGGC
 TCTTTTITACA AAGAAACAC ACCTTCCGAC CACGAGGTG GAGTGCAGG GAGACTTACC TTCTATTTTTT GGACGACCAC AGAACTGACG AGACGGTCCG
 1801 AATCCTGAAC ATTTGGGCAT GAAGAGCTAA AGTCTTTGGG TCTTGTTTAA CTCCTATTAC TGTCCTCCAAA TTCCCTCTAGT CCCTTGGGTC ATGATTAAAC
 TTAGGACTTG TAAACCCGTA CTTCTCGATT TCAGAAACCC AGAACAAATT GAGGATAATG ACAGGGGTTT AAGGGATCA GGGAAACCCAG TACTAATTG
 1901 ATTTTGACTT AAAAAA AAAA AAAA
 TAAACTGAA TTTTTTTTTT TTTTTTTTTT TTTTTT

FIGURE 1B